

Alpha Virus nsp3 alignment

CLUSTAL W (1.82) multiple sequence alignment

SFV_nsp3	APSYRVKRADIATCTEAAVNAANARGTVGDVCRAVAKKWPASFKAATPVGTTKTVMC	60
ONV_nsp3	APSYRVKRMDIAKNTTEECVVNAANPRGVPGDGVCKAVYRKWPESFRNSATPGTAKTMC	60
RRV_nsp3	APSYRVRTDISGHAEAVNAANAKGTVGVCRARWKPDFFKGAAATPGTAKLVQA	60
SinV_nsp3	APSYRTKRENIADCQEEAVVNAANPLGRPGEGVCRAYKRWPTSFTDSATETGTARMTVC	60
VEEV_nsp3	APSYHVVVRGDIATATEGVIINAANSKGQPGGGVCGALYKKFPESFDLQPIEVGKARLVKG	60
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SFV_nsp3	GSYPVIHAVAPNFSATTEAEGDRELAAVYRAVAAEVNRLSLSVAIPLLSTGVFSGGDR	120
ONV_nsp3	GQYPVIHAVGPNFNSNYSEAEVDRELASVYREVAKEVSRGLGVSSVAIPLLSTGVYSGKDR	120
RRV_nsp3	NGMNVIHAVGPNFSTVTEAEGDRELAAAYRAVAGIINASNICKSVAIPLLSTGVFSGGDR	120
SinV_nsp3	LGKKVIHAVGPDFRKHPEAEALKLLQNAYHAVADLVNEHNICKSVAIPLLSTGIYAAGKDR	120
VEEV_nsp3	AAKIIHAVGPNFNKVSEVEGDKQLAEAYESIAKIVNDNNYKSVAIPLLSTGIFSGNKDR	120
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SFV_nsp3	LQOSLNHLFTAMDADVTIYCRDKSWEKKIQEADMRNAV-ELLNDD---VELTTL	175
ONV_nsp3	LLQSLNHLFAAMDSTDADVVIYCRDKEWEKKITEAISLRSQV-ELLDHH---ISVDCDI	175
RRV_nsp3	VMQSLNHLFTAMDADVVIYCRDKAWEKKIQEADRRNAV-ELVSED---ISLESDL	175
SinV_nsp3	LEVSLNCLTTALDRTDADVTIYCLDKKKWERIDAALQLKESVTELKDED---MEIDDEL	176
VEEV_nsp3	LTQSLNHLTTALDTTADVAIYCRDKKWEMLKEAVARREAVEEICISDDSSVTEPDAEL	180
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SFV_nsp3	VRVHPDSSLVGRKGYSTTDGSLYSYFEGTKFNQAAIDMAEILTLWPRLOEANERICLYAL	235
ONV_nsp3	VRVHPDSSLAGRKGYSTVEGALYSYLEGTRFHQTAVDMAE IYTMWPQTEANEQVCLYAL	235
RRV_nsp3	IRVHPDSCLVGRKGYSITDGKLHSYLEGTRFHQTAVDMAE ISTLWPKLQDANEQICLYAL	235
SinV_nsp3	VWIHPDSCLKGRKGFFTTKGKLYSYFEGTKFHQAACKDMAEIKVLFPNQESNEQLCAYIL	236
VEEV_nsp3	VRVHPKSSLAGRKGYSTSDGKTFSYLEGTKFHQAACKDIAEINAMWPVATEANEQVCMYIL	240
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SFV_nsp3	GETMDNIGSKCPVNDSDSSTPPRTVPCLCRYAMTAERIARLRSHQVKSMVVCSSFPLPKY	295
ONV_nsp3	GESIESVRQKCPVDDADASFPPKTVPCLCRYAMTPERVARLRMNHTTSIIVCSSFPLPKY	295
RRV_nsp3	GESMDSIRTKCPVEDADSSTPPKTVPCLCRYAMTAERVARLRMNNTKAIIVCSSFPLPKY	295
SinV_nsp3	GETMEAIREKCPVDNPSSSPKTLPCLCMYAMTPERVHRLRSNNKEVTVCSSTPLPKH	296
VEEV_nsp3	GESMSSIRSKCPVEESEASTPPSTLPCLCIHAMTPERVQRLKASRPEQITVCSSFPLPKY	300
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SFV_nsp3	HVDGVQKVCEKVLFDPTVPSVSPRKYAAS----TTDHSDRSLRGF DLDWTTDSSST	350
ONV_nsp3	KIEGVQKVCSKALLFDHNVPSRVSPRTYRPADEI IQTPQTPTEACQDAQLVQSINDEAV	355
RRV_nsp3	RIEGVQKVCDRVLIFDQTVPSLVSPRKYIPAAASMHADTVSLDTVSTGSAWSFPSEAT	355
SinV_nsp3	KIKNVQVQCTKVLFNPHTPAFVPARKYIEVPE---QPTAPPQAEEAPEVVATPSPST	353
VEEV_nsp3	RITGVQKIQCSPQILFSPKVPAYIHPKYLVETPPVEETPESPAENQSTEQTPEQPALVN	360
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SFV_nsp3	-----ASDTMSLPSLQSCDIDSIVEPMAP-----IVVTADVHP----EPAGI	388
ONV_nsp3	PVPSDLEACDATMDWPSIGTVSTRQRHDSSDSEYSGRSRSNIQLVTADVHAPMYAHSLASS	415
RRV_nsp3	-YETMEVVAEVHHSEPPVPPP RRRRAQVTMHH-----QELLEVSDMHT----PIAAR	402
SinV_nsp3	ADNTSLDVDTDISLDMDSSSEGLSFSSFGSDN-----SITSMDWS----SGPSS	399
VEEV_nsp3	VDATRTRMPEPIIIEEEEEDSISLLSDGPTHQ-----VLQVEADIHG----SPSVS	407
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SFV_nsp3	ADLAADVHPEPADH----VDLEN-----PIPPPRPKRAAYLASRAAER-----	427
ONV_nsp3	GGSMSLSSPEAQNGTMILLDSEDTDSISRVSTPIAPPRLGRTINVTCDERE--GKIL	473
RRV_nsp3	VEIPVYDTAVVAER-VAIPCTSEY-----ATPIPTPRAVRRVPVPAPRIQRASYRVS	454
SinV_nsp3	LEIVDRRQVVVADV---HAVQEP-----APIPPPRLKMMARLAAARKEPTPPASNS	447
VEEV_nsp3	SSWSIIPHASFDFDVDSLISILDLDG-----ASVTSGAVSAETNSYFARSMEFRAR	457
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SFV_nsp3	PVPAPR-KPTPAPRTAFR-----NKLPLTFGDFDEHEVDAL--	462
ONV_nsp3	PMASDR-FFTAKPYTVALSVSTADMVYPIQAPLGLIPPP TLEPITFGDFAEGERIDNL--	530
RRV_nsp3	PTPTPR-VLRASVCSVTSAG----VEFPWA PEDLEVLT EPVHCEMREPVELPWEPE--	506
SinV_nsp3	SESLHL-SFGGVMSLGSIFDG---ETARQAAVQPLATGPTDVPMSFGSFSDGEIDE LSR	503
VEEV_nsp3	PVPAPRTVFRNPPHPAPRT RTP---PLAHSRASSRTSLVSTPPGVNRVITREEALTP	513

SFV_nsp3 ---ASG-ITFGDF-----DDVRLGRAGA--- 482
ONV_nsp3 ---LTGALTFGDFEPGEVEELTDSEWSTCSDTDEELRLDRAGG--- 570
RRV_nsp3 ---DVD-IQFGDFET-----PDKIQFGDIDFDQF 531
SinV_nsp3 RVTESEPVLFGSFEPGEVNSIISSSRSAVSFPLRKQRRRRRSRTEY 549
VEEV_nsp3 SRAPSRSAVRTSLVS-----NPPGVNRVITREEFEAFVAQQQ-- 550
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